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In the specification:

On page 1, lines 14-18 please cancel the Paragraph beginning at line 14 and replace it with the following paragraph:

--This application claims priority to U.S. Serial No. 60/287,724, filed May 2, 2001 and U.S. Provisional Application Ser. No. 60/221,607, filed on July 28, 2000. Incorporated by reference are U.S. Serial No. 60/287,724, filed May 2, 2001; U.S. Provisional Application Ser. No. 60/221,607, filed on July 28, 2000; and U.S. Application Ser. No. 09/133,987, filed on August 13, 1998.--

On Page 14, please replace the Paragraph beginning at line 5 as follows:

Referring to FIG. 1, a transcription unit or gene has, for example, three exons: A, B, and C, and is alternatively spliced in transcription giving rise to two variants: transcript 1 (AC) and transcript 2 (BC). An oligo complementaryeomplimentary to sequence A, or a fragment thereof, would therefore only detect transcript 1, not transcript 2. An oligo complimentary to sequence B or a fragment thereof, by contrast, would only detect transcript 2, not transcript 1.

On page 14, please replace the Paragraph that begins at line 19 as follows:

FIG. [[4]] 3 demonstrates a transcription unit or a gene that has 5 exons: A, B, 20 C, D, and E. There are four alternatively spliced transcripts: transcript 1 (ACD), 2 (ACE), 3 (BCD), and 4 (BCE). This is a more complex scheme but the principle remains the same: An oligo complementary to sequence A or a fragment thereof would be able to only detect transcripts 1 and 2 (hence "1+2=A"); an oligo complementary to sequence B would be able to only detect transcripts 3 and 4 (hence "3+4=B"); an oligo complementary to sequence D would be able to only detect transcripts 1 and 3 (hence "1+3=D"); and an oligo complimentary to sequence E would be able to only detect transcripts 2 and 4 (hence "2+4=E") Therefore, we have

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a number of oligos that can specifically detect a subset of the splice variants. And, additionally, resolving the four polyvariance equations above would reveal the level of abundance of each splice variant (A, B, D, and E). Moreover, an oligo complementary to sequence C or a fragment thereof would be able to detect all four transcripts and thus measure the total level of abundances of these splice variants.

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Objections to Embedded Hyperlink

The Examiner has objected to the hyperlinks presented on page 15. Applicant does not intend to have these hyperlinks be active links. Please disable these hyperlinks when preparing the text to be loaded onto the USPTO web database. It is noted that the instant patent application as published on the USPTO web database does not have these links enabled.